

Quantifying Information in a Phylogenetic Tree: The Robustness of Phylogenetic Signal

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Since Felsenstein (1985)'s influential paper on phylogenetic contrasts, phylogenetically-based inferences of evolutionary patterns have gotten increasingly more complex (Hansen, 1997; Butler and King, 2004; Freckleton and Harvey, 2006; O'Meara et al., 2006; Pagel and Meade, 2006). More and more sophisticated models are applied to datasets of species mean traits on a phylogenetic tree in an attempt to answer such questions as reconstructing ancestral states, identify changes in rates of character evolution across time and across clades, identify the number and location of evolutionary optima or the strength of stabilizing selection. In each of these analyses, an ultrametric phylogenetic tree is the only source of temporal information to quantify these intrinsically temporally-based questions.

The extent to which a phylogenetic tree can reliably shed light into the evolution of traits in the past depends not only on its size but on its structure. For instance, an unresolved or star phylogeny contains no information and renders phylogenetic techniques uninformative, regardless of the number of taxa. While the question of phylogenetic signal is not new (Price, 1997; Losos, 1996), there has been insufficient analysis of when a phylogenetic signal is substantial enough to inform the kinds of inferences we now routinely perform.

I will present examples of how typical phylogenetic analyses are applied to trees that are insufficiently informative to choose between models. I will discuss ways to detect and quantify the power of a phylogenetic tree relative to common methods. I will introduce an actively developing open source software package for addressing these issues. In the spirit of the conference, this research and code are being developed and released in the open under GPL-v3.0 and Creative Commons by-sa licenses.

- **Project Open Notebook:** http://openwetware.org/wiki/User:Carl_Boettiger/Notebook/Comparative_Phylogenetics
- **Project Open Code Development:** <http://github.com/cboettig/Comparative-Phylogenetics/>

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